

SEQUENCE LISTING

<110> KAPELLER-LIBERMANN
SILOS-SANTIAGO

<120> METHODS OF USING 18903 TO TREAT PAIN AND
PAIN-RELATED DISORDERS

<130> MNI-199

<150> 60/250929

<151> 2000-11-30

<160> 7

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1983

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (98)...(1849)

<400> 1

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                                         Met Pro Ser Thr Val Leu
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cca tcc aca gtg ttg cca tca ctc ctg ccc aca gca gga gct ggc tgg 163
Pro Ser Thr Val Leu Pro Ser Leu Leu Pro Thr Ala Gly Ala Gly Trp
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Ser Met Arg Trp Ile Leu Cys Trp Ser Leu Thr Leu Cys Leu Met Ala
          25           30           35

cag acg gcc ttg ggt gcc ttg cac acc aag agg cct caa gtg gtc acc 259
Gln Thr Ala Leu Gly Ala Leu His Thr Lys Arg Pro Gln Val Val Thr
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aaa tat gga acc ctg caa gga aaa cag atg cat gtg ggg aag aca ccc 307
Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met His Val Gly Lys Thr Pro
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atc caa gtc ttt tta gga gtc ccc ttc tcc aga cct cct cta ggt atc 355
Ile Gln Val Phe Leu Gly Val Pro Phe Ser Arg Pro Pro Leu Gly Ile
          75           80           85

ctc agg ttt gca cct cca gaa ccc ccg gag ccc tgg aaa gga atc aga 403
Leu Arg Phe Ala Pro Pro Glu Pro Pro Glu Pro Trp Lys Gly Ile Arg
          90           95           100

gat gct acc acc tac ccg cct ggg tgc ctg cag gag tcc tgg ggc cag 451
Asp Ala Thr Thr Tyr Pro Pro Gly Cys Leu Gln Glu Ser Trp Gly Gln
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ccc ggg gat ccc cag ctg cca gtg atg gtc tgg ttc ccg gga ggc gcc Pro Gly Asp Pro Gln Leu Pro Val Met Val Trp Phe Pro Gly Gly Ala 155 160 165	595
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cgc gag aaa gtg gtg ctg gtg ttt ctg cag cac agg ctc ggc atc ttc Arg Glu Lys Val Val Leu Val Phe Leu Gln His Arg Leu Gly Ile Phe 185 190 195	691
ggc ttc ctg agc acg gac gac agc cac gcg cgc ggg aac tgg ggg ctg Gly Phe Leu Ser Thr Asp Asp Ser His Ala Arg Gly Asn Trp Gly Leu 200 205 210	739
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ttc ggg gga gac cca gga aat gtg acc ctg ttc ggc cag tcg gcg ggg Phe Gly Gly Asp Pro Gly Asn Val Thr Leu Phe Gly Gln Ser Ala Gly 235 240 245	835
gcc atg agc atc tca gga ctg atg atg tca ccc cta gcc tcg ggt ctc Ala Met Ser Ile Ser Gly Leu Met Met Ser Pro Leu Ala Ser Gly Leu 250 255 260	883
ttc cat cgg gcc att tcc cag agt ggc acc gcg tta ttc aga ctt ttc Phe His Arg Ala Ile Ser Gln Ser Gly Thr Ala Leu Phe Arg Leu Phe 265 270 275	931
atc act agt aac cca ctg aaa gtg gcc aag aag gtt gcc cac ctg gct Ile Thr Ser Asn Pro Leu Lys Val Ala Lys Lys Val Ala His Leu Ala 280 285 290	979
gga tgc aac cac aac agc aca cag atc ctg gta aac tgc ctg agg gca Gly Cys Asn His Asn Ser Thr Gln Ile Leu Val Asn Cys Leu Arg Ala 295 300 305 310	1027
cta tca ggg acc aag gtg atg cgt gtg tcc aac aag atg aga ttc ctc Leu Ser Gly Thr Lys Val Met Arg Val Ser Asn Lys Met Arg Phe Leu 315 320 325	1075
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Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu Leu Gly Val Asn Asn	
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Leu Glu Phe Asn Trp Leu Leu Pro Tyr Ile Met Lys Phe Pro Leu Asn	
375 380 385 390	
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Arg Gln Ala Met Arg Lys Glu Thr Ile Thr Lys Met Leu Trp Ser Thr	
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cgc acc ctg ttg aat atc acc aag gag cag gta cca ctt gtg gtg gag	1363
Arg Thr Leu Leu Asn Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu	
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gag tac ctg gac aat gtc aat gag cat gac tgg aag atg cta cga aac	1411
Glu Tyr Leu Asp Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn	
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Arg Met Met Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu	
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Gln Thr Ala His Tyr His Arg Asp Ala Gly Leu Pro Val Tyr Leu Tyr	
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Glu Phe Glu His His Ala Arg Gly Ile Ile Val Lys Pro Arg Thr Asp	
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Gly Ala Asp His Gly Asp Glu Met Tyr Phe Leu Phe Gly Gly Pro Phe	
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Ala Thr Gly Leu Ser Met Gly Lys Glu Lys Ala Leu Ser Leu Gln Met	
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Asn Leu Pro Cys Trp Pro Arg Tyr Asn Lys Asp Glu Lys Tyr Leu Gln	
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Gln Phe	
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 <212> PRT
 <213> Homo sapiens

<400> 2

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His	Val	Gly	Lys	Thr	Pro	Ile	Gln	Val	Phe	Leu	Gly	Val	Pro	Phe	Ser
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Arg	Pro	Pro	Leu	Gly	Ile	Leu	Arg	Phe	Ala	Pro	Pro	Glu	Pro	Pro	Glu
			85						90					95	
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Trp	Phe	Pro	Gly	Gly	Ala	Phe	Ile	Val	Gly	Ala	Ala	Ser	Ser	Tyr	Glu
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Phe	Gly	Gln	Ser	Ala	Gly	Ala	Met	Ser	Ile	Ser	Gly	Leu	Met	Met	Ser
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Pro	Leu	Ala	Ser	Gly	Leu	Phe	His	Arg	Ala	Ile	Ser	Gln	Ser	Gly	Thr
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Lys	Val	Ala	His	Leu	Ala	Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile	Leu
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Asn	Lys	Met	Arg	Phe	Leu	Gln	Leu	Asn	Phe	Gln	Arg	Asp	Pro	Glu	Glu
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Ile	Ile	Trp	Ser	Met	Ser	Pro	Val	Val	Asp	Gly	Val	Val	Ile	Pro	Asp
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Asp	Pro	Leu	Val	Leu	Leu	Thr	Gln	Gly	Lys	Val	Ser	Ser	Val	Pro	Tyr
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Leu	Leu	Gly	Val	Asn	Asn	Leu	Glu	Phe	Asn	Trp	Leu	Leu	Pro	Tyr	Ile
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Met	Lys	Phe	Pro	Leu	Asn	Arg	Gln	Ala	Met	Arg	Lys	Glu	Thr	Ile	Thr
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Lys	Met	Leu	Trp	Ser	Thr	Arg	Thr	Leu	Leu	Asn	Ile	Thr	Lys	Glu	Gln
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Val	Pro	Leu	Val	Val	Glu	Glu	Tyr	Leu	Asp	Asn	Val	Asn	Glu	His	Asp
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Trp Lys Met Leu Arg Asn Arg Met Met Asp Ile Val Gln Asp Ala Thr
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 Phe Val Tyr Ala Thr Leu Gln Thr Ala His Tyr His Arg Asp Ala Gly
 450 455 460
 Leu Pro Val Tyr Leu Tyr Glu Phe Glu His His Ala Arg Gly Ile Ile
 465 470 475 480
 Val Lys Pro Arg Thr Asp Gly Ala Asp His Gly Asp Glu Met Tyr Phe
 485 490 495
 Leu Phe Gly Gly Pro Phe Ala Thr Gly Leu Ser Met Gly Lys Glu Lys
 500 505 510
 Ala Leu Ser Leu Gln Met Met Lys Tyr Trp Ala Asn Phe Ala Arg Thr
 515 520 525
 Gly Asn Pro Asn Asp Gly Asn Leu Pro Cys Trp Pro Arg Tyr Asn Lys
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 Thr Ala Gly Ala Gly Trp Ser Met Arg Trp Ile Leu Cys Trp Ser Leu
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 acc ctc tgc ctg atg gcg cag acg gcc ttg ggt gcc ttg cac acc aag 144
 Thr Leu Cys Leu Met Ala Gln Thr Ala Leu Gly Ala Leu His Thr Lys
 35 40 45
 agg cct caa gtg gtc acc aaa tat gga acc ctg caa gga aaa cag atg 192
 Arg Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met
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 cat gtg ggg aag aca ccc atc caa gtc ttt tta gga gtc ccc ttc tcc 240
 His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe Ser
 65 70 75 80
 aga cct cct cta ggt atc ctc agg ttt gca cct cca gaa ccc ccg gag 288
 Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro Pro Glu
 85 90 95
 ccc tgg aaa gga atc aga gat gct acc acc tac ccg cct ggg tgc ctg 336
 Pro Trp Lys Gly Ile Arg Asp Ala Thr Thr Tyr Pro Pro Gly Cys Leu
 100 105 110
 cag gag tcc tgg ggc cag ctg gcc tcg atg tac gtc agc acg cgg gaa 384

Gln	Glu	Ser	Trp	Gly	Gln	Leu	Ala	Ser	Met	Tyr	Val	Ser	Thr	Arg	Glu	
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cgg	tac	aag	tgg	ctg	cgc	ttc	agc	gag	gac	tgt	ctg	tac	ctg	aac	gtg	432
Arg	Tyr	Lys	Trp	Leu	Arg	Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	
	130					135					140					
tac	gcg	ccg	gcg	cgc	gcg	ccc	ggg	gat	ccc	cag	ctg	cca	gtg	atg	gtc	480
Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met	Val	
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ggc	tct	gac	ttg	gcc	gcc	cgc	gag	aaa	gtg	gtg	ctg	gtg	ttt	ctg	cag	576
Gly	Ser	Asp	Leu	Ala	Ala	Arg	Glu	Lys	Val	Val	Leu	Val	Phe	Leu	Gln	
			180					185					190			
cac	agg	ctc	ggc	atc	ttc	ggc	ttc	ctg	agc	acg	gac	gac	agc	cac	gcg	624
His	Arg	Leu	Gly	Ile	Phe	Gly	Phe	Leu	Ser	Thr	Asp	Asp	Ser	His	Ala	
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Arg	Gly	Asn	Trp	Gly	Leu	Leu	Asp	Gln	Met	Ala	Ala	Leu	Arg	Trp	Val	
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Gln	Glu	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp	Pro	Gly	Asn	Val	Thr	Leu	
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Phe	Gly	Gln	Ser	Ala	Gly	Ala	Met	Ser	Ile	Ser	Gly	Leu	Met	Met	Ser	
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Pro	Leu	Ala	Ser	Gly	Leu	Phe	His	Arg	Ala	Ile	Ser	Gln	Ser	Gly	Thr	
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Ala	Leu	Phe	Arg	Leu	Phe	Ile	Thr	Ser	Asn	Pro	Leu	Lys	Val	Ala	Lys	
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Lys	Val	Ala	His	Leu	Ala	Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile	Leu	
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Val	Asn	Cys	Leu	Arg	Ala	Leu	Ser	Gly	Thr	Lys	Val	Met	Arg	Val	Ser	
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aac	aag	atg	aga	ttc	ctc	caa	ctg	aac	ttc	cag	aga	gac	ccg	gaa	gag	1008
Asn	Lys	Met	Arg	Phe	Leu	Gln	Leu									

355	360	365	
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gta cca ctt gtg gtg gag gag tac ctg gac aat gtc aat gag cat gac Val Pro Leu Val Val Glu Glu Tyr Leu Asp Asn Val Asn Glu His Asp 420 425 430			1296
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gtc aaa ccc cgc act gat ggg gca gac cat ggg gat gag atg tac ttc Val Lys Pro Arg Thr Asp Gly Ala Asp His Gly Asp Glu Met Tyr Phe 485 490 495			1488
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gat gaa aag tac ctg cag ctg gat ttt acc aca aga gtg ggc atg aag Asp Glu Lys Tyr Leu Gln Leu Asp Phe Thr Thr Arg Val Gly Met Lys 545 550 555 560			1680
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<212> PRT

<213> Artificial Sequence

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<223> Xaa may be Gly or Arg

<221> VARIANT

<222> 4,5,6,7,9,11,13

<223> Xaa may be any amino acid

<221> VARIANT

<222> 8

<223> Xaa may be Leu, Ile, Met or Val

<221> VARIANT

<222> 10

<223> Xaa may be Leu, Ile or Val

<221> VARIANT

<222> 15

<223> Xaa may be Ser, Thr, Ala, or Gly

<400> 4

Phe Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Ser Xaa Gly
1 5 10 15

<210> 5

<211> 11

<212> PRT

<213> Artificial Sequence

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<223> Motif

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<223> Xaa may be Glu or Asp

<221> VARIANT

<222> 5

<223> Xaa may be Tyr or Thr

<221> VARIANT

<222> 6,8

<223> Xaa may be Leu, Ile or Val

<221> VARIANT

<222> 7

<223> Asp, Asn, or Ser

<221> VARIANT

<222> 9

<223> Xaa may be Leu, Ile, Phe, Tyr, Trp or Val

<221> VARIANT

<222> (10)...(10)

<223> Xaa may be any amino acid

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<222> (11)...(11)

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Xaa Asp Cys Leu Xaa Xaa Xaa Xaa Xaa Xaa

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5

10

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<212> DNA

<213> Homo sapiens

<220>

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